



SEQUENCE LISTING

<110> Guss, Bengt
Nilsson, Martin
Frykberg, Lars
Flock, Jan-Ingmar
Lindberg, Martin

<120> Fibrinogen Binding Protein Originating from
Coagulase-Negative Staphylococcus

<130> guss 09/147405

<140> 09/147405

<141> 1999-04-01

<150> PCT/SE97/10191

<151> 1997-06-18

<150> SE 9602496-3

<151> 1996-06-20

<160> 15

<170> PatentIn Ver. 2.0

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<213> Artificial Sequence

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Val Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile
20 25 30

att aaa aaa gaa gaa acg aat aac tac gat ggc ata gaa aaa cgc tca 143
Ile Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser
35 40 45

gaa gat aga aca gag tca aca aca aat gta gat gaa aac gaa gca aca 191
Glu Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr
50 55 60

ttt tta caa aag acc cct caa gat aat act cat ctt aca gaa gaa gag 239
Phe Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu
65 70 75

gta aaa gaa tcc tca tca gtc gaa tcc tca aat tca tca att gat act 287

Val Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr	
80 85 90 95	
gcc caa caa cca tct cac aca aca ata aat aga gaa gaa tct gtt caa	335
Ala Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln	
100 105 110	
aca agt gat aat gta gaa gat tca cac gta tca gat ttt gct aac tct	383
Thr Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser	
115 120 125	
aaa ata aaa gag agt aac act gaa tct ggt aaa gaa gag aat act ata	431
Lys Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile	
130 135 140	
gag caa cct aat aaa gta aaa gaa gat tca aca aca agt cag ccg tct	479
Glu Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser	
145 150 155	
ggc tat aca aat ata gat gaa aaa att tca aat caa gat gag tta tta	527
Gly Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu	
160 165 170 175	
aat tta cca ata aat gaa tat gaa aat aag gct aga cca tta tct aca	575
Asn Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr	
180 185 190	
aca tct gcc caa cca tcg att aaa cgt gta acc gta aat caa tta gcg	623
Thr Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala	
195 200 205	
gcg gaa caa ggt tcg aat gtt aac cat tta att aaa gtt act gat caa	671
Ala Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr Asp Gln	
210 215 220	
agt att act gaa gga tat gat gat agt gaa ggt gtt att aaa gca cat	719
Ser Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His	
225 230 235	
gat gct gaa aac tta atc tat gat gta act ttt gaa gta gat gat aag	767
Asp Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys	
240 245 250 255	
gtg aaa tct ggt gat acg atg aca gtg gat ata gat aag aat aca gtt	815
Val Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn Thr Val	
260 265 270	
cca tca gat tta acc gat agc ttt aca ata cca aaa ata aaa gat aat	863

Pro	Ser	Asp	Leu	Thr	Asp	Ser	Phe	Thr	Ile	Pro	Lys	Ile	Lys	Asp	Asn	
			275					280					285			
tct	gga	gaa	atc	atc	gct	aca	ggt	act	tat	gat	aac	aaa	aat	aaa	caa	911
Ser	Gly	Glu	Ile	Ile	Ala	Thr	Gly	Thr	Tyr	Asp	Asn	Lys	Asn	Lys	Gln	
		290					295				300					
atc	acc	tat	act	ttt	aca	gat	tat	gta	gat	aag	tat	gaa	aat	att	aaa	959
Ile	Thr	Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Asp	Lys	Tyr	Glu	Asn	Ile	Lys	
	305					310				315						
gca	cac	ctt	aaa	tta	acg	tca	tac	att	gat	aaa	tca	aag	ggt	cca	aat	1007
Ala	His	Leu	Lys	Leu	Thr	Ser	Tyr	Ile	Asp	Lys	Ser	Lys	Val	Pro	Asn	
320					325				330						335	
aat	aat	acc	aag	tta	gat	gta	gaa	tat	aaa	acg	gcc	ctt	tca	tca	gta	1055
Asn	Asn	Thr	Lys	Leu	Asp	Val	Glu	Tyr	Lys	Thr	Ala	Leu	Ser	Ser	Val	
			340					345				350				
aat	aaa	aca	att	acg	ggt	gaa	tat	caa	aga	cct	aac	gaa	aat	cgg	act	1103
Asn	Lys	Thr	Ile	Thr	Val	Glu	Tyr	Gln	Arg	Pro	Asn	Glu	Asn	Arg	Thr	
		355					360					365				
gct	aac	ctt	caa	agt	atg	ttt	aca	aat	ata	gat	acg	aaa	aat	cat	aca	1151
Ala	Asn	Leu	Gln	Ser	Met	Phe	Thr	Asn	Ile	Asp	Thr	Lys	Asn	His	Thr	
	370					375					380					
ggt	gag	caa	acg	att	tat	att	aac	cct	ctt	cgt	tat	tca	gcc	aag	gaa	1199
Val	Glu	Gln	Thr	Ile	Tyr	Ile	Asn	Pro	Leu	Arg	Tyr	Ser	Ala	Lys	Glu	
	385					390				395						
aca	aat	gta	aat	att	tca	ggg	aat	ggt	gat	gaa	ggt	tca	aca	att	ata	1247
Thr	Asn	Val	Asn	Ile	Ser	Gly	Asn	Gly	Asp	Glu	Gly	Ser	Thr	Ile	Ile	
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Asp	Asp	Ser	Thr	Ile	Ile	Lys	Val	Tyr	Lys	Val	Gly	Asp	Asn	Gln	Asn	
			420					425				430				
tta	cca	gat	agt	aac	aga	att	tat	gat	tac	agt	gaa	tat	gaa	gat	gtc	1343
Leu	Pro	Asp	Ser	Asn	Arg	Ile	Tyr	Asp	Tyr	Ser	Glu	Tyr	Glu	Asp	Val	
		435					440				445					
aca	aat	gat	gat	tat	gcc	caa	tta	gga	aat	aat	aat	gat	gtg	aat	att	1391
Thr	Asn	Asp	Asp	Tyr	Ala	Gln	Leu	Gly	Asn	Asn	Asn	Asp	Val	Asn	Ile	
	450					455					460					
aat	ttt	ggt	aat	ata	gat	tca	cca	tat	att	att	aaa	ggt	att	agt	aaa	1439

Asn Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile Ser Lys	
465 470 475	
tat gac cct aat aag gat gat tac acg act ata cag caa act gtg aca	1487
Tyr Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr Val Thr	
480 485 490 495	
atg cag acg act ata aat gag tat act ggt gag ttt aga aca gca tcc	1535
Met Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser	
500 505 510	
tat gat aat aca att gct ttc tct aca agt tca ggt caa gga caa ggt	1583
Tyr Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly	
515 520 525	
gac ttg cct cct gaa aaa act tat aaa atc gga gat tac gta tgg gaa	1631
Asp Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu	
530 535 540	
gat gta gat aaa gat ggt att caa aat aca aat gat aat gaa aaa ccg	1679
Asp Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro	
545 550 555	
ctt agt aat gta ttg gta act ttg acg tat cct gat gga act tca aaa	1727
Leu Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys	
560 565 570 575	
tca gtc aga aca gat gaa gat ggg aaa tat caa ttt gat ggg gtg cag	1775
Ser Val Arg Thr Asp Glu Asp Gly Lys Tyr Gln Phe Asp Gly Val Gln	
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Val Asp	

<210> 11
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 <212> PRT
 <213> Staphylococcus epidermidis

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 Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser Glu

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Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr Phe		
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Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu Val		
65	70	75
Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr Ala		
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Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln Thr		
	100	105
Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser Lys		
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Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile Glu		
	130	135
Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser Gly		
145	150	155
Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn		
	165	170
Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr Thr		
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Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala Ala		
	195	200
Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr Asp Gln Ser		
	210	215
Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His Asp		
225	230	235
Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys Val		
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Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn Thr Val Pro		
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Ser Asp Leu Thr Asp Ser Phe Thr Ile Pro Lys Ile Lys Asp Asn Ser		
	275	280
Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln Ile		

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Thr	Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Asp	Lys	Tyr	Glu	Asn	Ile	Lys	Ala
305					310					315					320
His	Leu	Lys	Leu	Thr	Ser	Tyr	Ile	Asp	Lys	Ser	Lys	Val	Pro	Asn	Asn
				325					330					335	
Asn	Thr	Lys	Leu	Asp	Val	Glu	Tyr	Lys	Thr	Ala	Leu	Ser	Ser	Val	Asn
			340					345					350		
Lys	Thr	Ile	Thr	Val	Glu	Tyr	Gln	Arg	Pro	Asn	Glu	Asn	Arg	Thr	Ala
		355					360					365			
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Pro	Asp	Ser	Asn	Arg	Ile	Tyr	Asp	Tyr	Ser	Glu	Tyr	Glu	Asp	Val	Thr
		435					440					445			
Asn	Asp	Asp	Tyr	Ala	Gln	Leu	Gly	Asn	Asn	Asn	Asp	Val	Asn	Ile	Asn
		450				455					460				
Phe	Gly	Asn	Ile	Asp	Ser	Pro	Tyr	Ile	Ile	Lys	Val	Ile	Ser	Lys	Tyr
465					470					475					480
Asp	Pro	Asn	Lys	Asp	Asp	Tyr	Thr	Thr	Ile	Gln	Gln	Thr	Val	Thr	Met
			485					490						495	
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			500					505					510		
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		515					520				525				
Leu	Pro	Pro	Glu	Lys	Thr	Tyr	Lys	Ile	Gly	Asp	Tyr	Val	Trp	Glu	Asp
	530					535					540				
Val	Asp	Lys	Asp	Gly	Ile	Gln	Asn	Thr	Asn	Asp	Asn	Glu	Lys	Pro	Leu

545		550		555		560									
Ser	Asn	Val	Leu	Val	Thr	Leu	Thr	Tyr	Pro	Asp	Gly	Thr	Ser	Lys	Ser
				565					570					575	
Val	Arg	Thr	Asp	Glu	Asp	Gly	Lys	Tyr	Gln	Phe	Asp	Gly	Val	Gln	Val
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 gaagatagaa cagagtcaac aacaaatgta gatgaaaacg aagcaacatt ttacaaaag 180
 acccctcaag ataataactca tcttacagaa gaagaggtaa aagaatcctc atcagtcgaa 240
 tcctcaaatt catcaattga tactgcccaa caaccatctc acacaacaat aaatagagaa 300
 gaatctgttc aaacaagtga taatgtagaa gattcacacg tatcagattt tgctaactct 360
 aaaataaaa agagtaacac tgaatctggt aaagaagaga atactataga gcaacctaat 420
 aaagtaaaa aagattcaac aacaagtcag cegtctggct atacaaatat agatgaaaaa 480
 atttcaaadc aagatgagtt attaaattta ccaataaatg aatatgaaaa taaggctaga 540
 ccattatcta caacatctgc ccaaccatcg attaaacgtg taaccgtaaa tcaattagcg 600
 gcggaacaag gttcgaatgt taaccattta attaaagtta ctgatcaaag tattactgaa 660
 ggatatgatg atagtgaagg tgttattaaa gcacatgatg ctgaaaactt aatctatgat 720
 gtaacttttg aagtagatga taaggtgaaa tctggtgata cgatgacagt ggatatagat 780
 aagaatacag ttccatcaga tttaaccgat agctttacaa taccaaaaat aaaagataat 840
 tctggagaaa tcatcgctac aggtacttat gataacaaaa ataaacaaat cacctatact 900

tttacagatt atgtagataa gtatgaaaat attaaagcac accttaaatt aacgtcatat 960
 attgataaat caaagggtcc aaataataat accaagttag atgtagaata taaaacggcc 1020
 ctttcatcag taaataaaac aattacgggt gaatatcaaa gacctaacga aaatcggact 1080
 gctaaccttc aaagtatggt tacaatatata gatacgaaaa atcatacagt tgagcaaacy 1140
 atttatatta accctcttcg ttattcagcc aaggaaacaa atgtaaatat ttcaggggaat 1200
 ggtgatgaag gttcaacaat tatagacgat agcacaataa ttaaagttta taagggttga 1260
 gataatcaaa atttaccaga tagtaacaga atttatgatt acagtgaata tgaagatgtc 1320
 acaaatgatg attatgcccc attaggaaat aataatgatg tgaatattaa ttttggtaat 1380
 atagattcac catatattat taaagttatt agtaaatatg accctaataa ggatgattac 1440
 acgactatac agcaaactgt gacaatgcag acgactataa atgagtatac tgggtgagttt 1500
 agaacagcat cctatgataa tacaattgct ttctctacaa gttcaggtca aggacaaggt 1560
 gacttgcttc ctgaaaaaac ttataaaatc ggagattacg tatgggaaga ttagataaaa 1620
 gatggtattc aaaatacaaa tgataatgaa aaaccgctta gtaatgtatt ggtaactttg 1680
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 gatgga 1746

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 <213> *Staphylococcus epidermidis*

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 20 25 30
 Tyr Asp Gly Ile Glu Lys Arg Ser Glu Asp Arg Thr Glu Ser Thr Thr
 35 40 45
 Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr Pro Gln Asp
 50 55 60

Asn	Thr	His	Leu	Thr	Glu	Glu	Glu	Val	Lys	Glu	Ser	Ser	Ser	Val	Glu	65	70	75	80
Ser	Ser	Asn	Ser	Ser	Ile	Asp	Thr	Ala	Gln	Gln	Pro	Ser	His	Thr	Thr	85	90	95	
Ile	Asn	Arg	Glu	Glu	Ser	Val	Gln	Thr	Ser	Asp	Asn	Val	Glu	Asp	Ser	100	105	110	
His	Val	Ser	Asp	Phe	Ala	Asn	Ser	Lys	Ile	Lys	Glu	Ser	Asn	Thr	Glu	115	120	125	
Ser	Gly	Lys	Glu	Glu	Asn	Thr	Ile	Glu	Gln	Pro	Asn	Lys	Val	Lys	Glu	130	135	140	
Asp	Ser	Thr	Thr	Ser	Gln	Pro	Ser	Gly	Tyr	Thr	Asn	Ile	Asp	Glu	Lys	145	150	155	160
Ile	Ser	Asn	Gln	Asp	Glu	Leu	Leu	Asn	Leu	Pro	Ile	Asn	Glu	Tyr	Glu	165	170	175	
Asn	Lys	Ala	Arg	Pro	Leu	Ser	Thr	Thr	Ser	Ala	Gln	Pro	Ser	Ile	Lys	180	185	190	
Arg	Val	Thr	Val	Asn	Gln	Leu	Ala	Ala	Glu	Gln	Gly	Ser	Asn	Val	Asn	195	200	205	
His	Leu	Ile	Lys	Val	Thr	Asp	Gln	Ser	Ile	Thr	Glu	Gly	Tyr	Asp	Asp	210	215	220	
Ser	Glu	Gly	Val	Ile	Lys	Ala	His	Asp	Ala	Glu	Asn	Leu	Ile	Tyr	Asp	225	230	235	240
Val	Thr	Phe	Glu	Val	Asp	Asp	Lys	Val	Lys	Ser	Gly	Asp	Thr	Met	Thr	245	250	255	
Val	Asp	Ile	Asp	Lys	Asn	Thr	Val	Pro	Ser	Asp	Leu	Thr	Asp	Ser	Phe	260	265	270	
Thr	Ile	Pro	Lys	Ile	Lys	Asp	Asn	Ser	Gly	Glu	Ile	Ile	Ala	Thr	Gly	275	280	285	
Thr	Tyr	Asp	Asn	Lys	Asn	Lys	Gln	Ile	Thr	Tyr	Thr	Phe	Thr	Asp	Tyr	290	295	300	
Val	Asp	Lys	Tyr	Glu	Asn	Ile	Lys	Ala	His	Leu	Lys	Leu	Thr	Ser	Tyr	305	310	315	320

Ile	Asp	Lys	Ser	Lys	Val	Pro	Asn	Asn	Asn	Thr	Lys	Leu	Asp	Val	Glu	325	330	335	
Tyr	Lys	Thr	Ala	Leu	Ser	Ser	Val	Asn	Lys	Thr	Ile	Thr	Val	Glu	Tyr	340	345	350	
Gln	Arg	Pro	Asn	Glu	Asn	Arg	Thr	Ala	Asn	Leu	Gln	Ser	Met	Phe	Thr	355	360	365	
Asn	Ile	Asp	Thr	Lys	Asn	His	Thr	Val	Glu	Gln	Thr	Ile	Tyr	Ile	Asn	370	375	380	
Pro	Leu	Arg	Tyr	Ser	Ala	Lys	Glu	Thr	Asn	Val	Asn	Ile	Ser	Gly	Asn	385	390	395	400
Gly	Asp	Glu	Gly	Ser	Thr	Ile	Ile	Asp	Asp	Ser	Thr	Ile	Ile	Lys	Val	405	410	415	
Tyr	Lys	Val	Gly	Asp	Asn	Gln	Asn	Leu	Pro	Asp	Ser	Asn	Arg	Ile	Tyr	420	425	430	
Asp	Tyr	Ser	Glu	Tyr	Glu	Asp	Val	Thr	Asn	Asp	Asp	Tyr	Ala	Gln	Leu	435	440	445	
Gly	Asn	Asn	Asn	Asp	Val	Asn	Ile	Asn	Phe	Gly	Asn	Ile	Asp	Ser	Pro	450	455	460	
Tyr	Ile	Ile	Lys	Val	Ile	Ser	Lys	Tyr	Asp	Pro	Asn	Lys	Asp	Asp	Tyr	465	470	475	480
Thr	Thr	Ile	Gln	Gln	Thr	Val	Thr	Met	Gln	Thr	Thr	Ile	Asn	Glu	Tyr	485	490	495	
Thr	Gly	Glu	Phe	Arg	Thr	Ala	Ser	Tyr	Asp	Asn	Thr	Ile	Ala	Phe	Ser	500	505	510	
Thr	Ser	Ser	Gly	Gln	Gly	Gln	Gly	Asp	Leu	Pro	Pro	Glu	Lys	Thr	Tyr	515	520	525	
Lys	Ile	Gly	Asp	Tyr	Val	Trp	Glu	Asp	Val	Asp	Lys	Asp	Gly	Ile	Gln	530	535	540	
Asn	Thr	Asn	Asp	Asn	Glu	Lys	Pro	Leu	Ser	Asn	Val	Leu	Val	Thr	Leu	545	550	555	560
Thr	Tyr	Pro	Asp	Gly	Thr	Ser	Lys	Ser	Val	Arg	Thr	Asp	Glu	Asp	Gly	565	570	575	

Lys Tyr Gln Phe Asp Gly
580

<210> 14
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<212> DNA
<213> *Staphylococcus epidermidis*

<220>
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Ile Arg Lys Phe Thr Val Gly Thr Ala Ser Ile Val Ile Gly Ala Thr
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Val Gln Asp Val Lys Asp Ser Asn Thr Asp Asp Glu Leu Ser Asp Ser
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Asn Asp Gln Ser Ser Asp Glu Glu Lys Asn Asp Val Ile Asn Asn Asn
75 80 85

cag tca ata aac acc gac gat aat aac caa ata att aaa aaa gaa gaa 341
Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile Ile Lys Lys Glu Glu
90 95 100

acg aat aac tac gat ggc ata gaa aaa cgc tca gaa gat aga aca gag 389
Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser Glu Asp Arg Thr Glu
105 110 115

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Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr	
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Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu Val Lys Glu Ser Ser	
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Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile Glu Gln Pro Asn Lys	
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Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser Gly Tyr Thr Asn Ile	
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Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn Leu Pro Ile Asn	
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Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His Asp Ala Glu Asn Leu	
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Tyr Ile Asn Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile	
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Ile Lys Val Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn	
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Ala	Gln	Leu	Gly	Asn	Asn	Asn	Asp	Val	Asn	Ile	Asn	Phe	Gly	Asn	Ile	
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Asp	Asp	Tyr	Thr	Thr	Ile	Gln	Gln	Thr	Val	Thr	Met	Gln	Thr	Thr	Ile	
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Asn	Glu	Tyr	Thr	Gly	Glu	Phe	Arg	Thr	Ala	Ser	Tyr	Asp	Asn	Thr	Ile	
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Ser	Gly	Thr	Asn	Pro	Ala	Leu	Asp	Ser	Glu	Gly	Asn	Ser	Val	Trp	Val	
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Thr Leu Lys Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Thr Thr Asp	
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Glu Asn Gly Lys Tyr Gln Phe Asp Asn Leu Asn Ser Gly Asn Tyr Ile	
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Val His Phe Asp Lys Pro Ser Gly Met Thr Gln Thr Thr Thr Asp Ser	
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Gly Asp Asp Asp Glu Gln Asp Ala Asp Gly Glu Glu Val His Val Thr	
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Ile Thr Asp His Asp Asp Phe Ser Ile Asp Asn Gly Tyr Tyr Asp Asp	
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Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser	
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Ser Thr Lys Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp Tyr Gly	
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tct aaa ggc acg tta ctt gga act ctg ttt gca ggt tta gga gcg tta	3269
Ser Lys Gly Thr Leu Leu Gly Thr Leu Phe Ala Gly Leu Gly Ala Leu	
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 Ala Lys Ala Glu Glu Asn Ser Val Gln Asp Val Lys Asp Ser Asn Thr
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 Asp Asp Glu Leu Ser Asp Ser Asn Asp Gln Ser Ser Asp Glu Glu Lys
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 85 90 95
 Gln Ile Ile Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys
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 Arg Ser Glu Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu
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 Ala Thr Phe Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu
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 Glu Glu Val Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile

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Val Gln Thr Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala						
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Asn Ser Lys Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn						
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Thr Ile Glu Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln						
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Pro Ser Gly Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu						
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Leu Ala Ala Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr						
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Asp Gln Ser Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys						
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Asp Lys Val Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn						
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Thr Val Pro Ser Asp Leu Thr Asp Ser Phe Thr Ile Pro Lys Ile Lys						
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Asp Asn Ser Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn						
		355		360		365
Lys Gln Ile Thr Tyr Thr Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asn						
		370		375		380
Ile Lys Ala His Leu Lys Leu Thr Ser Tyr Ile Asp Lys Ser Lys Val						
		385		390		395
						400
Pro Asn Asn Asn Thr Lys Leu Asp Val Glu Tyr Lys Thr Ala Leu Ser						

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705	710	715
Val Trp Tyr Asp Thr Asn Lys Asp Gly Ile Gln Gly Asp Asp Glu Lys		
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Gly Ile Ser Gly Val Lys Val Thr Leu Lys Asp Glu Asn Gly Asn Ile		
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755	760	765
Leu Asn Ser Gly Asn Tyr Ile Val His Phe Asp Lys Pro Ser Gly Met		
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Asp Asn Gly Tyr Tyr Asp Asp Glu Ser Asp Ser Asp Ser Asp Ser Asp		
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Gly Ala Asn Glu Asp Tyr Gly Ser Lys Gly Thr Leu Leu Gly Thr Leu		
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